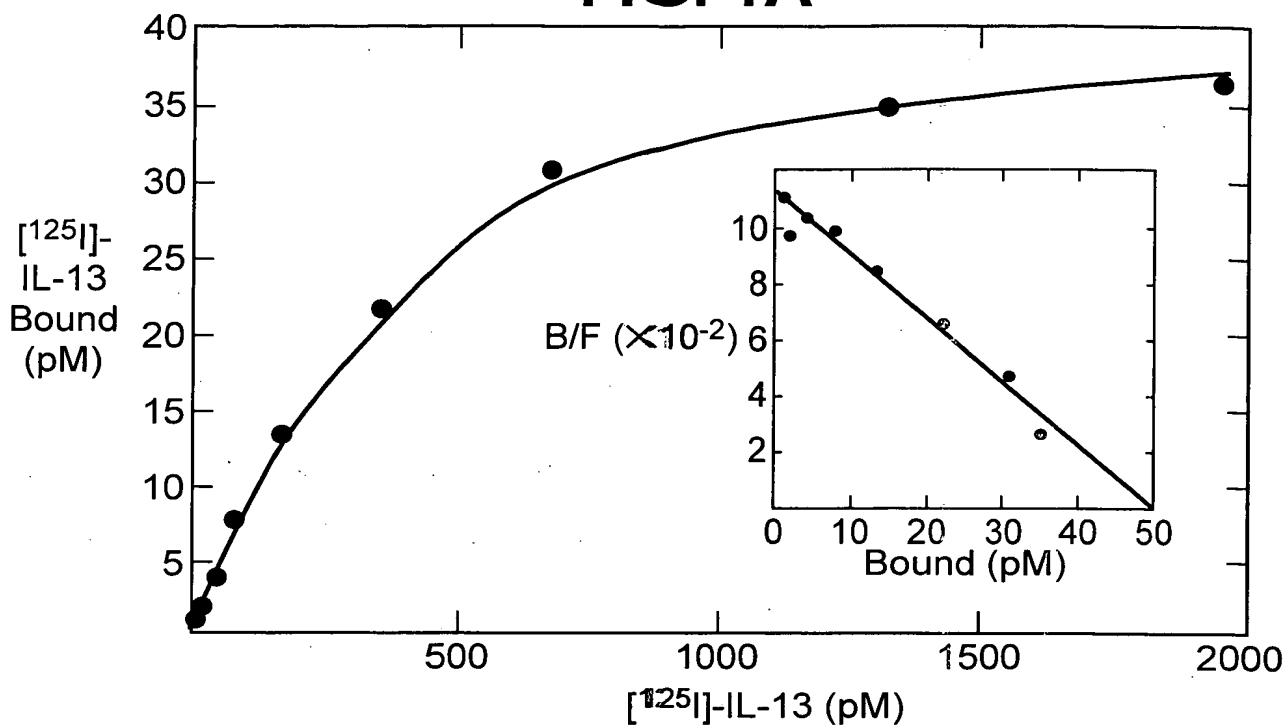
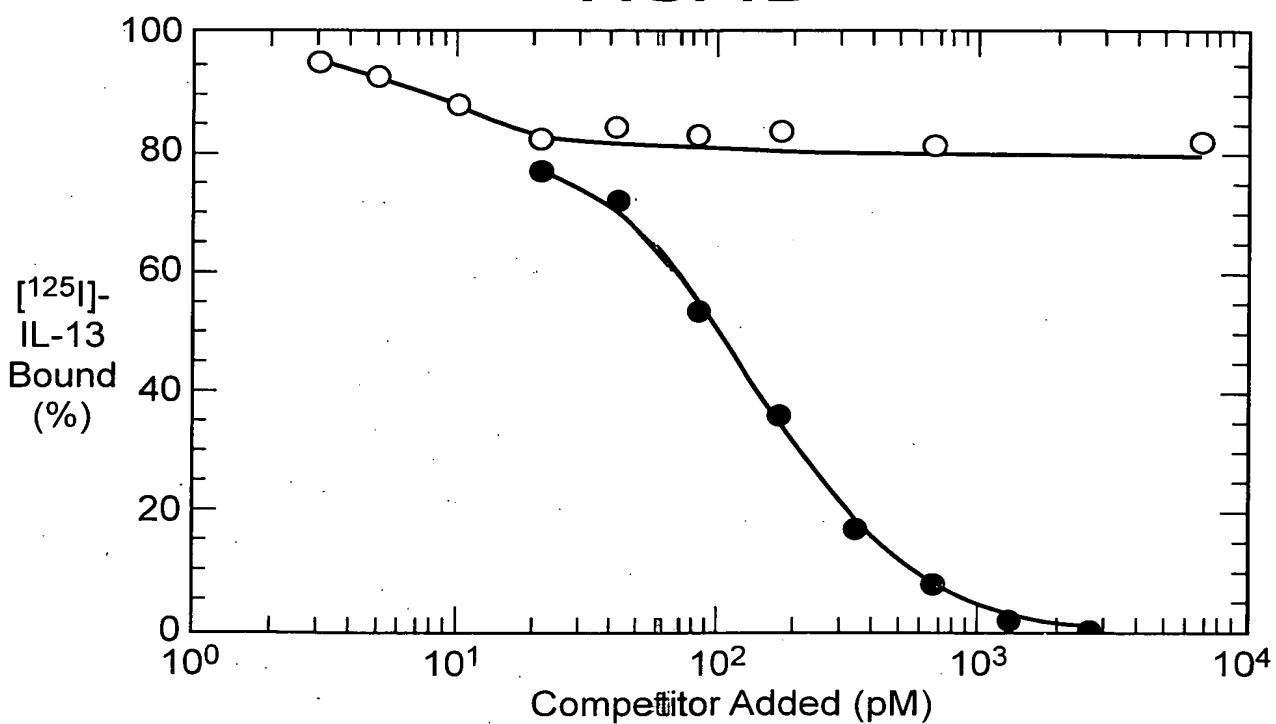


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**FIG. 1A**

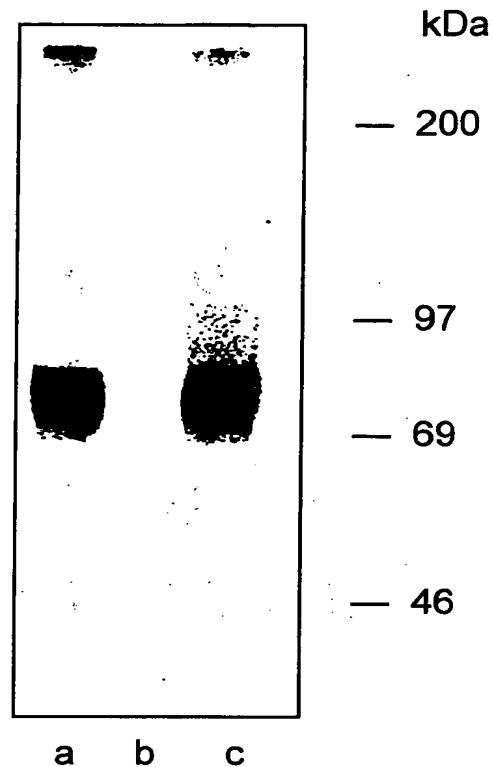


**FIG. 1B**



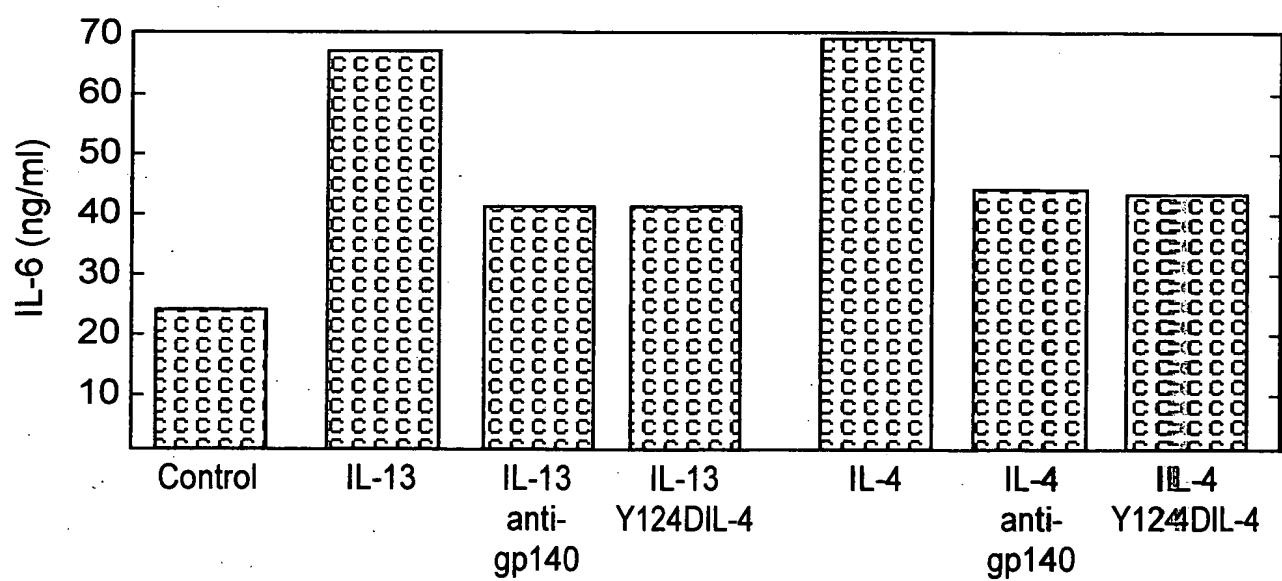
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**FIG. 1C**



a    b    c

**FIG. 1D**



**FIG. 2A**

1	GGTGCCTGGCGGGAGAGGCAATTATCAAGGTTAAATCTCGAGAAATGGCT	58
59	TTCGTTTGCTTGGCATCGGATGCTTATAACCTTCTGATAAGCACACATTTGGCTGT PheValCysLeuAlaTlieGlyCysLeuTyrThrPheLeuIleSerThrPheGlyCys	22
119	ACTTCATCTCAGACACCAGATAAAAGTTAACCCCTCAGGATTGAGATAAGTAGTGGAT ThrSerSerSerAspThrGluIleLysValAsnProProGlnAspPheGluIleValAsp	42
179	CCCGATTAAGTTAGGTTATCTCTTGCATGGCAAACCCCCACTGTCTGGATCATTT ProGlyTyrLeuGlyTyrLeuTyrLeuGlnTrpGlnProProLeuSerLeuAspHisPhe	238
143	AAGGAATGGCACAGTGGAAATAACTAAACTAAATGAAACATGGATTGAGTAGTGAACATGGAA LysGlucCysThrValGluIleLysTyrArgAsnIleGlySerGluThrTrpLys	62
239	ACCATTACCAAGAATCTACATTACAAGATGGTTGATCTTAACAAAGGCCATTGAA ThrIleThrLysAsnLeuHistYrLysAspGlyPheAspLeuAsnLysGlyIleGlu	298
63	GGAAAGATACACACGCTTTACATGGCAATGCACAAATGGATCAGAAGTTCAAAGTCC AlaLysThrIleHisThrLeuProTrpGlnCysThrAsnGlySerGluValGlnSerSer	82
299	TGGGCAGAAACTTACCTTGGATATTGGATATCACCACAAAGGAATTCCAGAAACTAAAGTTCAGGAT TrpAlaGluThrThrTyrTrpIleSerProGlnGlyIleProGluThrLysValGlnAsp	358
83	ATGGATTTGGCTATATTACAATTGGCAATTTACTGTTCTGGAAACCTGGCATAGGT MetAspCysValTyrTyrAsnTrpGlnTyrLeuCysSerTrpLysProGlyIleGly	102
359	GTAATTGATAACCAATTACAACATTGGTATTGAGGGCTTGGATCATGCATTA ValLeuAspThrAsnTyrAsnLeuPheTyrTrpTyrGluGlyLeuAspHisAlaLeu	418
103	TGGGCAGAAACTTACCTTGGATATTGGATATCACCACAAAGGAATTCCAGAAACTAAAGTTCAGGAT TrpAlaGluThrThrTyrTrpIleSerProGlnGlyIleProGluThrLysValGlnAsp	122
419	ATGGATTTGGCTATATTACAATTGGCAATTTACTGTTCTGGAAACCTGGCATAGGT MetAspCysValTyrTyrAsnTrpGlnTyrLeuCysSerTrpLysProGlyIleGly	478
123	GTAATTGATAACCAATTACAACATTGGTATTGAGGGCTTGGATCATGCATTA ValLeuAspThrAsnTyrAsnLeuPheTyrTrpTyrGluGlyLeuAspHisAlaLeu	142
479	TGGGCAGAAACTTACCTTGGATATTGGCAATTTACTGTTCTGGAAACCTGGCATAGGT MetAspCysValTyrTyrAsnTrpGlnTyrLeuCysSerTrpLysProGlyIleGly	538
143	GTAATTGATAACCAATTACAACATTGGTATTGAGGGCTTGGATCATGCATTA ValLeuAspThrAsnTyrAsnLeuPheTyrTrpTyrGluGlyLeuAspHisAlaLeu	162
539	CAGTGTGTTGATTACATCAAGGCTGATGGACAAATAAGGATGGCAGATTCCCATTG GlnCysValAspTyrIleGlyCysArgPheProTyrLeu	598
163		182
599		658
183		202

## FIG. 2B

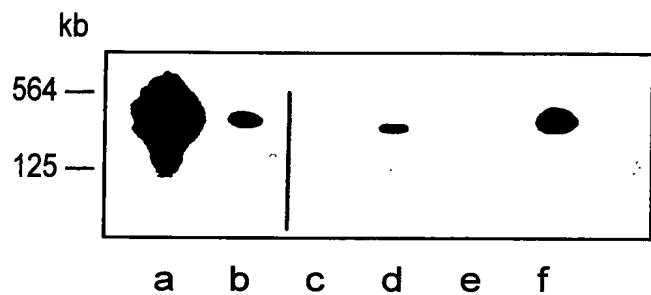
659	GAGGCATCAGACTATAAAGATTCTATTTGTGTTAAATGGATCATCAGAGAACAGCCT	718
203	GluAlaSerAspTyrLysAspPheTyrIleCysVal <u>AsnGlySer</u> GluAsnLysPro	222
719	ATCAGATCCAGTTATTCACTTTCAGCTTCAAATAATAGTTAAACCTTTGCCGCCAGTC	778
223	IleArgSerSerTyrPheThrPheGlnLeuGlnAsnIleVallysProLeuProProVal	242
779	TATCTTACTTTACTCGGGAGAGTGTGAATTAAAGCTGAAATGGAGCATACCTTTG	838
243	TyrLeuThrPheThrArgGluSerSerCysGluIleLysLeuLysLeuLysIleProLeu	262
839	GGACCTTATTCCAGCAAAGGTGTTTGATTATGAAATTGAGATCAGAGAAGATGATACTACC	898
263	GLYProIleProAlaArgCysPheAspTyrGluIleGluIleArgGluAspAspThrThr	282
899	TTGGTGACTGCTACAGTTGAAATGAAACATACACACCTTGAAAACAATGAAACCCGA	958
283	LeuValThrAlaThrValGlu <u>AsnGlu</u> ThrThrLeuLysThr <u>AsnGlu</u> ThrArg	302
959	CAATTATGCTTTGTAGTAAGGAAGCAAAGTGAATATTGCTCAGATGACCGGAATTGG	1018
303	GlnLeuCysPheValValArgSerLysValAsnIleTyrcysSerAspAspGlyIleTrp	322
1019	AGTGAGTGGAGTATAAACAAATGCTGGGAAGGGTGAAGAACCTATCGAAGAAACTTTGCTA	1078
323	SerGluTrpSerAspLysGlnCysStrpGluGlyGluAspLeuSerLysThrLeuLeu	342
1079	CGTTTCTGGCTTACCATTTGTTCATCTTAATATTAGTTGTAACCGGTCTGCTT	1138
343	Arg <b>Phe</b> Ter <b>Phe</b> Gly <b>Phe</b> Ile <b>Leu</b> Val <b>Ile</b> <b>Leu</b> <b>Val</b> <b>Ile</b> <b>Phe</b> <b>Val</b> <b>Thr</b> <b>Gly</b> <b>Leu</b> <b>Leu</b>	362
1139	TTGCGTAAGCCAAACACCTACCCAAAAATGATTCCAGAAATTGTTCTGTGATACATGAAGA	1198
363	<b>Leu</b> ArgLysProAsnThrTyrProLysMetIleProGluPhePheCysAspThr	380
1199	CTTCCATATCAAGAGACATGGTATTGACTCAACAGTTCCAGTCATGCCAAATGTTCA	1258
1259	ATATGAGTCTCAATAAACACTGAATTGGAAATGTTG	1298

**FIG. 2C**

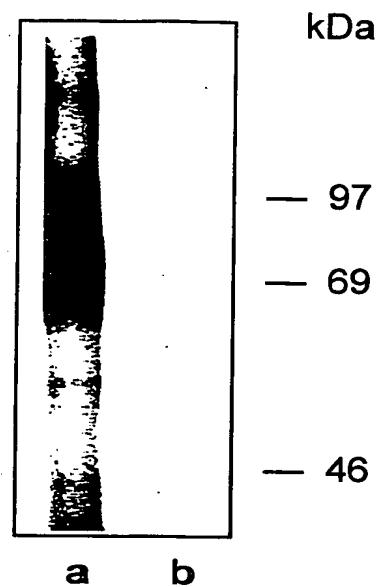
## FIG. 2D

IL13R	KPLPPVYLFFRESSCCEIKLKWSTIPLGPIPARCFDYIEIREDDTILVTA	286
IL5R	QINPPLMNVTAEIEGT.RLSIOWEKPVSAAFPIHCFDYEVKIHNTRNGYLIQI	286
IL13R	TVENETYTTLKTTNETRQLCFVVRSKVNTIYCSDDGIWSEWSDKQCWEGEDL	336
IL5R	EKLMTNAFISIIDDLSKYDVQVRRAVSSMCREAGIWSEWSQ.PIYVGNDDE	335
IL13R	SKKTLLRFWLPEFGFILILVIFVTGLLRKPNTYPKMIPI.....EF	376
IL5R	HKPLREWFVIVIMATICFILLSLICKICHLWIKLFPPIDAPKSNIKDL	385
IL13R	FCDT.....	380
IL5R	FVTTNYEKAGSSETIEVICCYIEKPGVETLEDHSVF	420

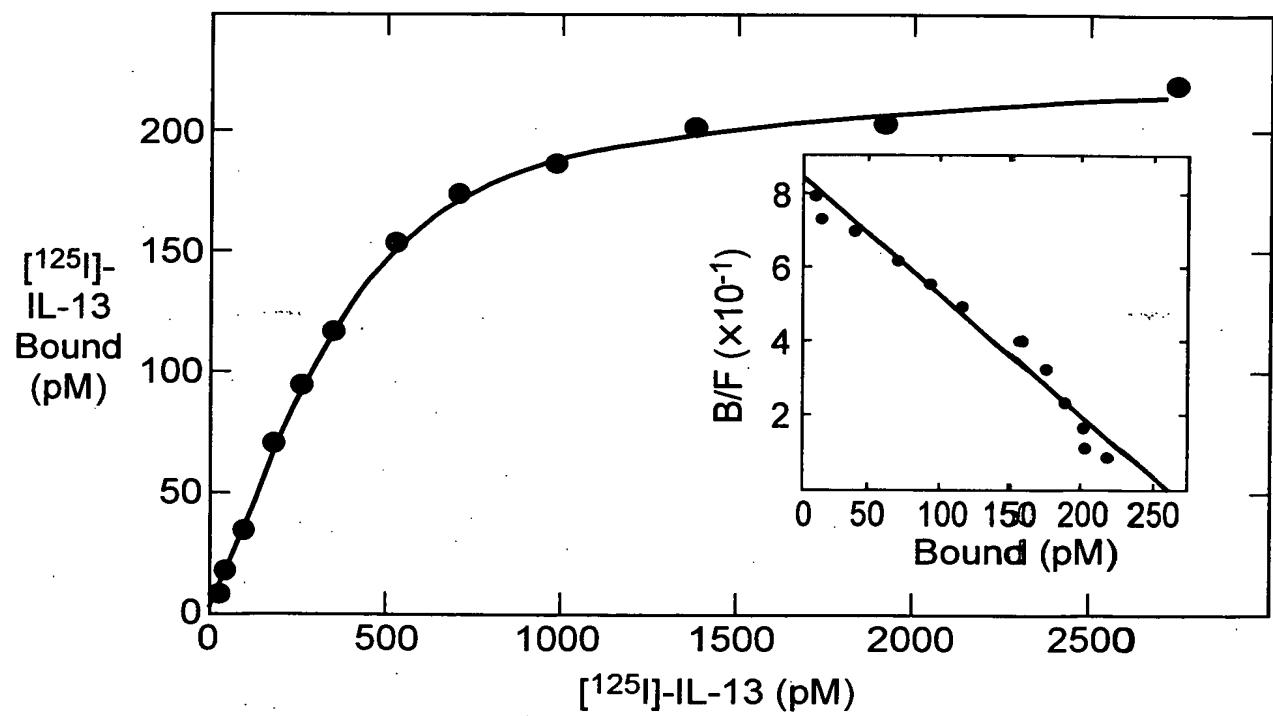
**FIG. 3**



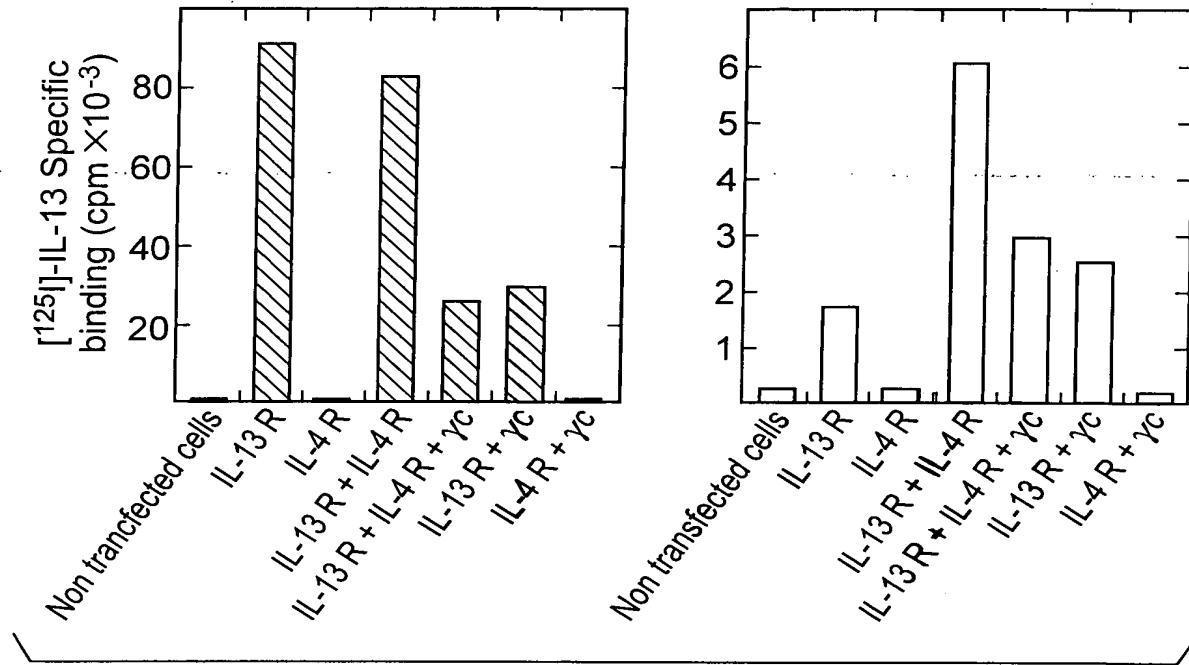
**FIG. 4B**



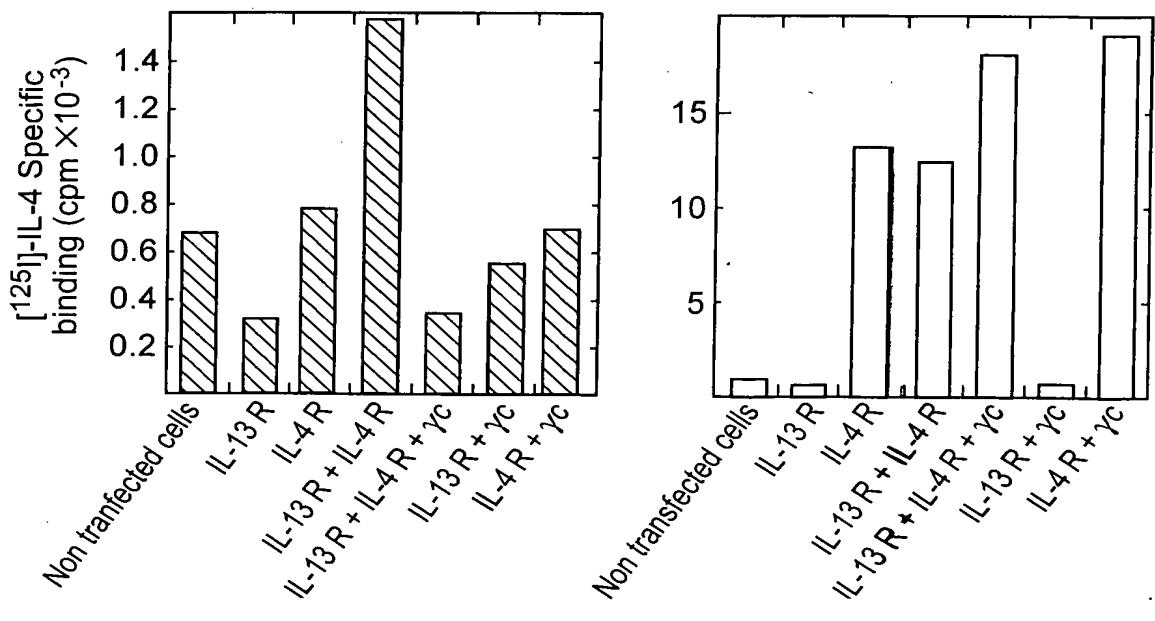
**FIG. 4A**



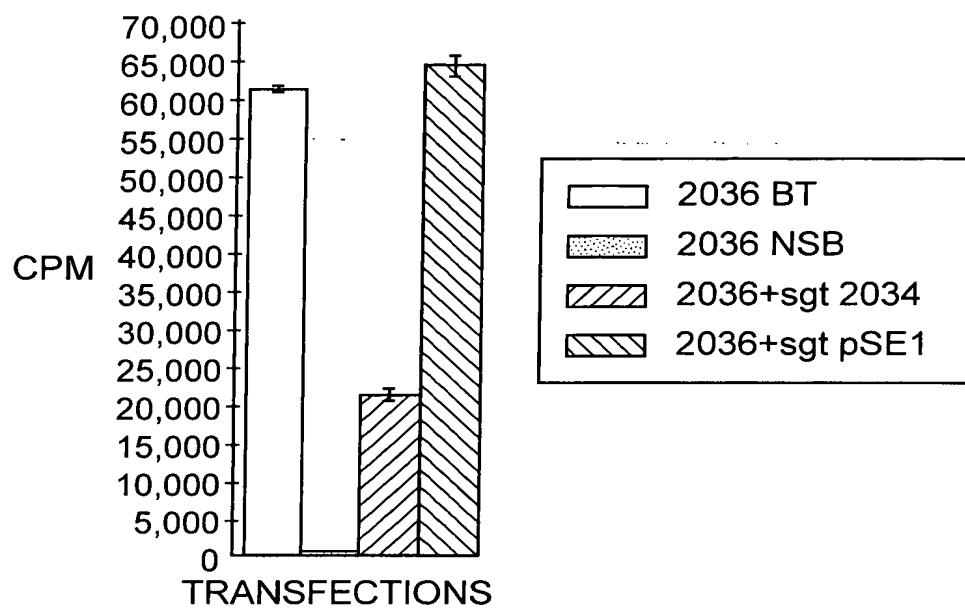
**FIG. 4C**



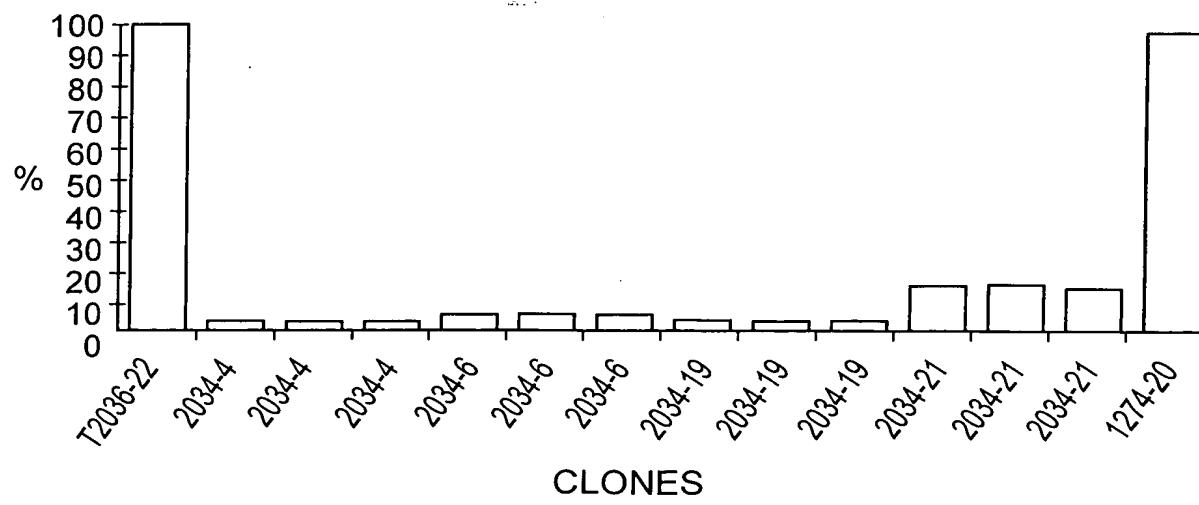
**FIG. 4D**



**FIG. 5**



**FIG. 6**



**FIG. 7A**

## FIG. 7B

61 GCAGGAAAATTAAACCATCCTTCAATATACTGCCTTTAACCTCCCGTGTGAAACCTGAT  
 10 A G K I K P S F N I V P L T S R V K P D 229  
 21 CCTCCACATATTAAACCTCTCCCTCACATTGACCTATATGTGCAATGGGAGAAT  
 30 P P H I K N L S E H N D D L Y V Q W E N 249  
 41 CCACAGAATTAGCAGATGCCTATTATGAAGTAGAAGTCAATAACAGGCCAACT 780  
 50 P Q N F I S R C L F Y E V E V N N S Q T 840  
 61 GAGACACATAATGTTTCTACGGTCCAAGAGGCTAAATGTGAGAATCCAGAATTGAGAGA 900  
 70 E T H N V F Y V Q E A K C E N P E F E R 269  
 81 AATGTGGAGAATACATCTTGTTCATGGTCCCTGGTGTCTCCTGATACTTTGAGACA 960  
 90 N V E N T S C F M V P G V L P D T L N T 309  
 100 GTCAGAATAAGAGTCAAACAAATAAGTTATGCTATGAGGATGACAAACTCTGGAGTAAT 1020  
 10 V R I R V K T N K L C Y E D D K L W S N 329  
 110 TGGAGCCAAAGAAATGAGTATAGGTAAGGAAGGCCAATTCCACACTCTACATAACCATTGTTA 1080  
 120 W S Q E M S I G K R N S T L Y I T M L 349  
 130 CTCATTGTTCCAGTCATCGTCCAGGTGCAATCATAGTACTCCTGCTTACCTAAAAAGG 1140  
 140 L I V P V I V A G A I I V L L Y L K R 369  
 150 CTCAGATTATTCCCTCCAATTCCCTGATCCCTGGCAAGATTTAAAGAAATGTTT 1200  
 160 L K I I F P P I P D P G K I F K E M F 389  
 170 GGAGACCAGAATGATGATACTCTGCACGGAAAGTACGACATCTATGAGAAGCAAACC 1260  
 180 G D Q N D D T L H W K K Y D I Y E K Q T 409  
 190 AAGGAGGAAACCGACTCTGTAGTGCTGATAGAAAACCTGAAGAAAGCCTCTCAGTGATGG 1320  
 200 K E E T D S V V L I E N L K K A S Q \* 429

**FIG. 7C**

81 TATCTGGGAACCTTAAATGGAAACTGACCATTAAACAGGCAGCTC  
41 ATAAGGCCACAGGTCTTATGTTGAGTCATTCTCATTAATGGCGCT  
01 TTGGAGAAGAGTGTGGAGTCATTCTCATTAATGGAGCTTCAAAACTAG  
61 GGGACAAAAGCAAAAGTGTGATGATACTGGTTGGAGTTAACATGGCT  
21 CCCTGAGGGATCTATACTGGCTTGTGTTCTTGTGCAACATGAACAAATTATTGT  
81 AGGGAACTCATTTGGGTGCAAATGCTAATGTCAAACTTGAGTCACAAAGAACATGTAG  
41 AAAACAAATGGATAAAATCTGATATGTATTGTTGGATCCTATTGAAACCATTGTTGTG  
01 GCTATTAAACTCTTTAACAGTCTGGCTGGCTGGCTCACGGCTGTAAATCCAG  
61 CAATTGGAGTCCGAGGCCGGGATCACTCGAGGTCAAGGAGTTCCAGGACTGAC  
21 CAAATGGTGAACCTCCTACTAAACTACAAATTAACACTGGGTGGGGCG  
81 TGCCTGTAATCCCAGCTACTCGGGAAAGCTGAGGAGGTGAATTGTTGAACCTGGAGGT  
41 GGAGGTTGCAGTGAGCAGAGATCACACCACCTGCACTCTAGCCTGGGTGACAGAGCAAGAC  
TCTGTCATAAAACAAAACAAAACAAAACAAAACAAAACAAAAC  
41 CATCATCCCCCTCGACAGCATTTCCTCTGCTTGAAGCCCCAGAAATCAGTGTGGCC  
21 ATGATGACAACACAGAGCCAGGCTTCTGGTATTAGAGTTCAACCATG  
81 TTAGGCTGTTAGGGCAGTGGAGGTAGAATGACCTGGTATTAGAGTTCAACCATG  
41 AAGCTCTAACAAATGTAATTTCACCTCTGCTACTCAAGTAGCATTACTGTCCTT  
01 GTTTGTGCTAGGCCCGGGGTGTGAAGCACAGACCCCTCCAGGGTTACAGTCTATT  
61 TGAGACTCCTCAGTCTGCCACTTTTAAATCTCCACOAGTCATTTCAGACCT  
21 TTAACTCCTCAATTCCAACACTGATTCCCCGTTGCATTCCCTCCCTCCT  
81 GTAGCCCTTGACTIONTCATTGGAAATTAGGATGTAATCTGCTCAGGAGACCTGGAGGAG  
41 CAGAGGATAATTAGCATCTCAGGTTAAGTGTGAGTAATTGAGAAACAAATGACTAATTCT  
01 TGCATATTGTAACCTCCATGTTGAGGGTTCAAGCATATTGTCATTCTAA

## FIG. 7D

61 CAGAGATGAGGTGATCTCACGTAACATTGGTATTGGCTTGAGAAAAAGAATAG  
21 TTGAACCTATTCTTACAAGATGGTCCAGGATTCTCTTCTGCCATAA 2820  
81 ATGATTAAATAAGCTTTACATTGGTGTCTTACATTGGTAGCCAGCCAAAGGCTCTGTT 2880  
41 ATGCTTTGGGCATATATTGGGTCCATTCTCACCTATCCACAAACATAATCCGTAT 2940  
01 ATATCCCCTACTTACTTACTCCCCAAATTAAAGAAGTATGGAAATGAGGGCATT 3000  
61 CCCCAACCCCATTTCTCCTCACACAGACTCATATTACTGGTAGGAACCTTGGAAACT 3060  
21 TATTCCAAGTGTCAAACATTACCAATCATATAACAAATGATGCTATTGCAAT 3120  
81 TCCGTCTCCTAGGGGAGGATAAAGAAACCCCTCACTCTACAGTTGGGTACAAGT 3180  
41 GGCACACCTGCTTCCATGGCCGTGTAGAAGCATGGTGCCTGGCTTCCTGAGGAAGCTGG 3240  
01 GGTCATGACAATGGCAGATGTAAGTTATTCTTGAAAGTCAGATTGGGGCTGGGAGACAG 3300  
61 CCGTAGTAGATGAGATAATTCCAGGTATTGTCTAGAAAGAATAATTGGTTTCTCTGT 3360  
21 ATAGGAATGAGATAATTCCAGGTATTGTCTAGAAAGAATAATTGGAAAGCAAAACCCATGC 3420  
81 CTCCCCCCTAGCCATTACTGTTATCCTATTAGATGCCATGAAGAGGGATGGCTGTGAA 3480  
41 ATTCCCACAAACATTGATGCTGACAGTCATGCAGTCTGGAGTGGGAAGTGATCTTT 3540  
01 GTCCCCATCCTCTTCTTAGCAGTAAAATAGCTGAGGAAAGGGAGGAAAGGAAGT 3600  
61 TATGGGAATAACCTGTGGTGGTTGTGATCCCTAGGTCTGGAGCTCTGGAGGTGTCTGT 3660  
21 ATCAGTGATTCCCATCCCCCTGTGGAAATTAGTAGGCTCATTTACTGTTAGGTCTA 3720  
81 GCCTATGGGATTTCCTAACATAACCTAACCTAACATAAGCAAACCCAGTGTCAAGGATGGTCTT 3780  
41 ATTCTTCGTTCAAGTTAAGTTCCCTCATCTGGGCACTGAAGGATAATGTGAAACAA 3840  
01 TGTAAACATTGGTAGTCACCAGGGATTGTCTTAACTTCTATAGGAAA 3900  
61 GCTTGAGTAAATAATTGTCTTGTATGTCAACCCaaaaaaaaaaaaaa 4009  
3960

**FIG. 7E**

MEWPRLCGIWALLCAGGGGGAAAPPTETQOPPVNTNLSVSVENLCTVIW  
MARPALLGELLVLL..WTATVGQVAATEVQOPPVNTNLSVSVENLCTVIW

TWNPPPEGASSNCISLWYFSHFQDKQDKKKIAPETRRSIEVPLNERICLQVGSS  
TWSPPPEGASPNCTILRYFSHFDDQQDQDKKKIAPETHRKEELPLDEKICLQVGSS

QCSTNESEKPSILVEKCISPPEGDPESAVTELQCIWHNLSYMKGCSWLPG  
QCSANESEKPSPLVKKCISPPEGDPESAVTELKCIWHNLSYMKGCSWLPG

NTSPDTNYTLYYWHRSLEKIHQGENIFREGQYFGQSFDLTKVKDSSFEQH  
NTSPDTHYTLYYWWYSSILEKSRQGENIYREGQHIAQSFKLTKV.EPSFEHQ

SVQIMVKDNAGKIKPSFNTIVPLTSRVKPDPPHIKNLSEHNDLIVQWENP  
NVQIMVKDNAGKIRPSCKIVSLLT SYVKPDPPHIKHLILKNGALLVQWKNP

IL-13 $\alpha$  Mouse      IL-13 $\alpha$  Human

50 ←                  48 ←

101                    99                    149                    201                    198

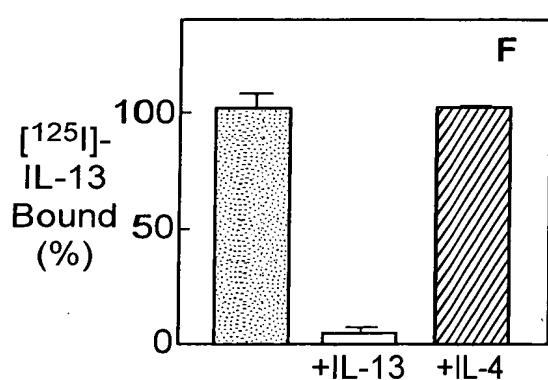
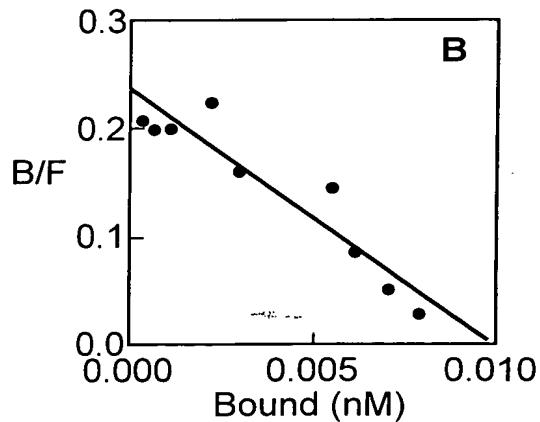
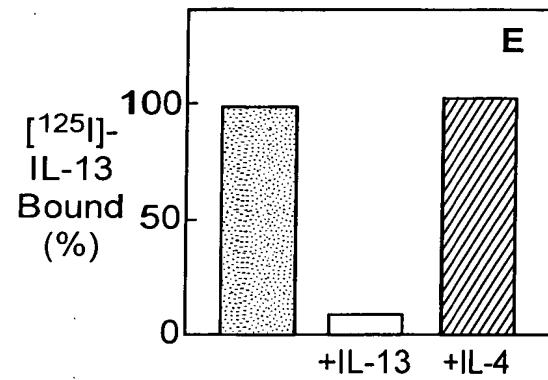
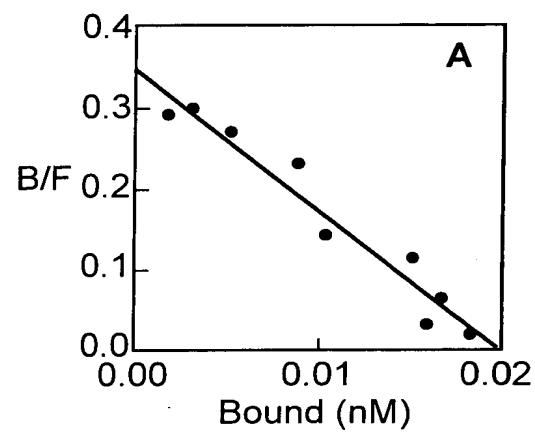
151                    149                    201                    250

100                    98                    148                    247

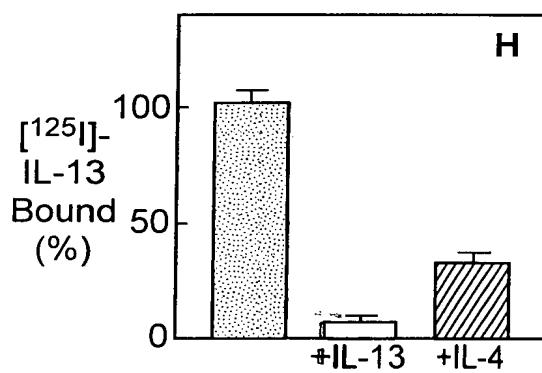
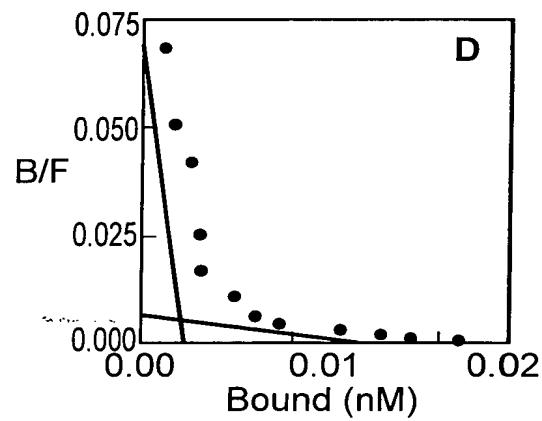
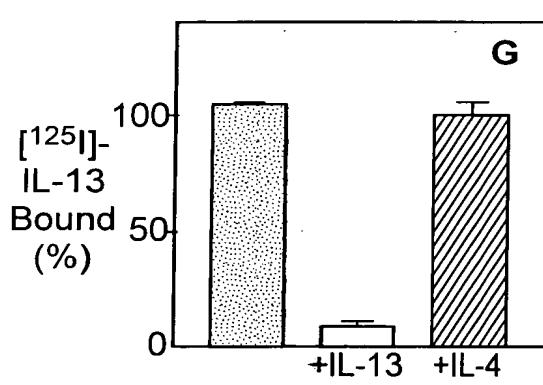
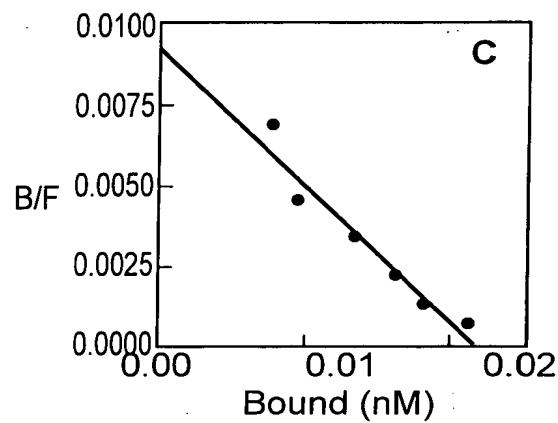
## FIG. 7F

	IL-13 $\alpha$ Mouse	IL-13 $\alpha$ Human
251	QNFISRCLFYEVENVNNSQTEETHNVFYVQEAKCENPEFERNNVENTSCEMVP	•
248	QNFRSRCCLTYEVENVNTQTDRHNILEVEEDKCQNSESDDRNMEGTSCFQLP	300 ← 297 ←
301	GVLPDITLNTRVIRVKTNKLGYEDDKLWNSNWQSQEMSIGKKRNSTLYITMILL	• 350
298	GVLADAVYTVRVRVKTNKLCFDDNKLNKLSDWSEAQSIGKEQNNSTFYTTMILL	347
351	TIPVIVAGAIIVLLLYLKRIKIIIFPPPIPDPGKIFKEMFGDQNDDTLHWRK	• 400
348	TIPVFVAVAVIILFYLKRIKIIIFPPPIPDPGKIFKEMFGDQNDDTLHWRK	397
401	KYDIYEKQTKEETDSVVLIENLKKASQ	427
398	KYDIYEKQSKEETDSVVLIENLKKAAP	424

**FIG. 8A**

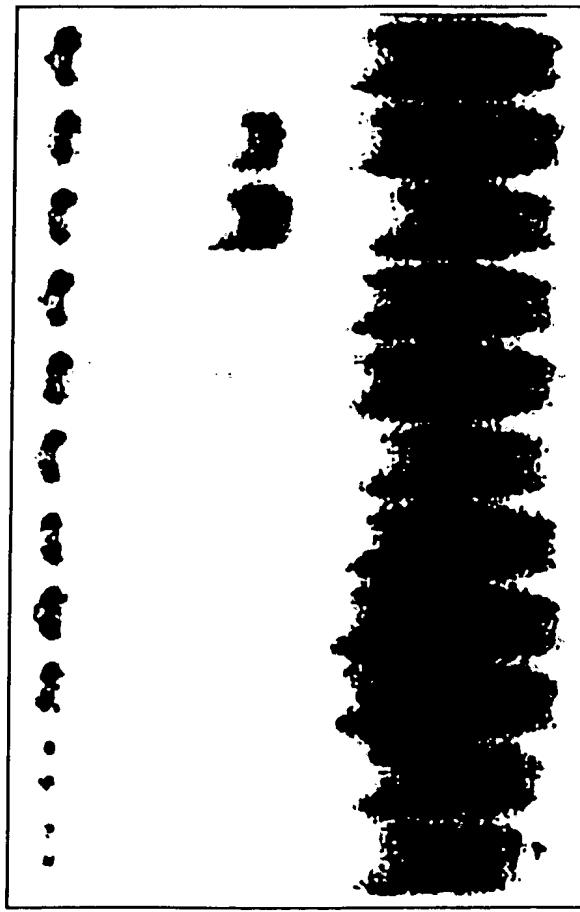


**FIG. 8B**



**FIG. 9**

CHO	CHO-4			CHO-13			CHO-4-13			
4	13	4	13	c	4	13	c	4	13	c
•	•	•	•	•	•	•	•	•	•	•



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